09/973,945
3/23/05

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 13, 2003, 09:50:40 ; Search time 1419 Seconds
(without alignments)
461.278 Million cell updates/sec

Title: US-09-973-945A-9
Perfect score: 16
Sequence: 1 gaatatatatatattc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16	100.0	103	9	HS46A3F	Z55508 H.sapiens C
c	2	16	100.0	103	9	HS46A3F	Z55508 H.sapiens C
	3	16	100.0	558	11	G81093	G81093 S208P6414RC
c	4	16	100.0	558	11	G81093	G81093 S208P6414RC
	5	16	100.0	566	11	BV070170	BV070170 S208P6211
c	6	16	100.0	566	11	BV070170	BV070170 S208P6211
	7	16	100.0	653	8	IMA295790	AJ295790 Isolepis
c	8	16	100.0	653	8	IMA295790	AJ295790 Isolepis
	9	16	100.0	5728	6	AX345003	AX345003 Sequence
c	10	16	100.0	5728	6	AX345003	AX345003 Sequence
	11	16	100.0	6059	9	AB023158	AB023158 Homo sapi
c	12	16	100.0	6059	9	AB023158	AB023158 Homo sapi
	13	16	100.0	6059	9	AY037299	AY037299 Homo sapi
c	14	16	100.0	6059	9	AY037299	AY037299 Homo sapi
	15	16	100.0	7733	3	DROAGPDHD	D50090 Drosophila
c	16	16	100.0	7733	3	DROAGPDHD	D50090 Drosophila
	17	16	100.0	7823	6	AX278034	AX278034 Sequence
c	18	16	100.0	7823	6	AX278034	AX278034 Sequence
	19	16	100.0	7823	6	AX323803	AX323803 Sequence
c	20	16	100.0	7823	6	AX323803	AX323803 Sequence
	21	16	100.0	7823	6	AX344488	AX344488 Sequence
c	22	16	100.0	7823	6	AX344488	AX344488 Sequence
	23	16	100.0	7823	6	AX346962	AX346962 Sequence
c	24	16	100.0	7823	6	AX346962	AX346962 Sequence
	25	16	100.0	8617	3	DMU19731	U19731 Drosophila
c	26	16	100.0	8617	3	DMU19731	U19731 Drosophila
	27	16	100.0	23501	9	AC126176	AC126176 Homo sapi
c	28	16	100.0	23501	9	AC126176	AC126176 Homo sapi
	29	16	100.0	23579	6	AX647373	AX647373 Sequence
c	30	16	100.0	23579	6	AX647373	AX647373 Sequence
	31	16	100.0	26246	3	CET12G3	Z68752 Caenorhabdi
c	32	16	100.0	26246	3	CET12G3	Z68752 Caenorhabdi
	33	16	100.0	28833	9	AC096581	AC096581 Homo sapi

c	34	16	100.0	28833	9	AC096581	AC096581 Homo sapi
	35	16	100.0	29682	2	AC012638	AC012638 Homo sapi
c	36	16	100.0	29682	2	AC012638	AC012638 Homo sapi
	37	16	100.0	30632	9	AL160051	AL160051 Human DNA
c	38	16	100.0	30632	9	AL160051	AL160051 Human DNA
	39	16	100.0	37566	9	AC068541	AC068541 Homo sapi
c	40	16	100.0	37566	9	AC068541	AC068541 Homo sapi
	41	16	100.0	38013	9	AL590287	AL590287 Human DNA
c	42	16	100.0	38013	9	AL590287	AL590287 Human DNA
	43	16	100.0	43581	9	AC005337	AC005337 Homo sapi
c	44	16	100.0	43581	9	AC005337	AC005337 Homo sapi
	45	16	100.0	44447	2	AC100099	AC100099 Mus muscu

ALIGNMENTS

RESULT 1
HS46A3F
LOCUS HS46A3F 103 bp DNA linear PRI 17-OCT-1995
DEFINITION H.sapiens CpG island DNA genomic Mse1 fragment, clone 46a3, forward read cpg46a3.ft1a.
ACCESSION Z55508
VERSION Z55508.1 GI:1021549
KEYWORDS CpG island; genomic Mse1 fragment.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column
JOURNAL Nat. Genet. 6 (3), 236-244 (1994)
MEDLINE 94282070
PUBMED 8012384
REFERENCE 2 (bases 1 to 103)
AUTHORS MacDonald,M., Huckle,E., Wilkinson,P. and Micklem,G.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
COMMENT Vector: pGEM-5Zf(-)
Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.
FEATURES Location/Qualifiers
source 1. .103
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="46a3"
/sex="male"
/tissue_type="blood"
/clone_lib="CGI-1"
/dev_stage="adult"
BASE COUNT 36 a 7 c 16 g 44 t
ORIGIN